



# results of BLAST

## BLASTN 2.2.11 [Jun-05-2005]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1124291504-12319-167553306596.BLASTQ2

### Query=

(48 letters)

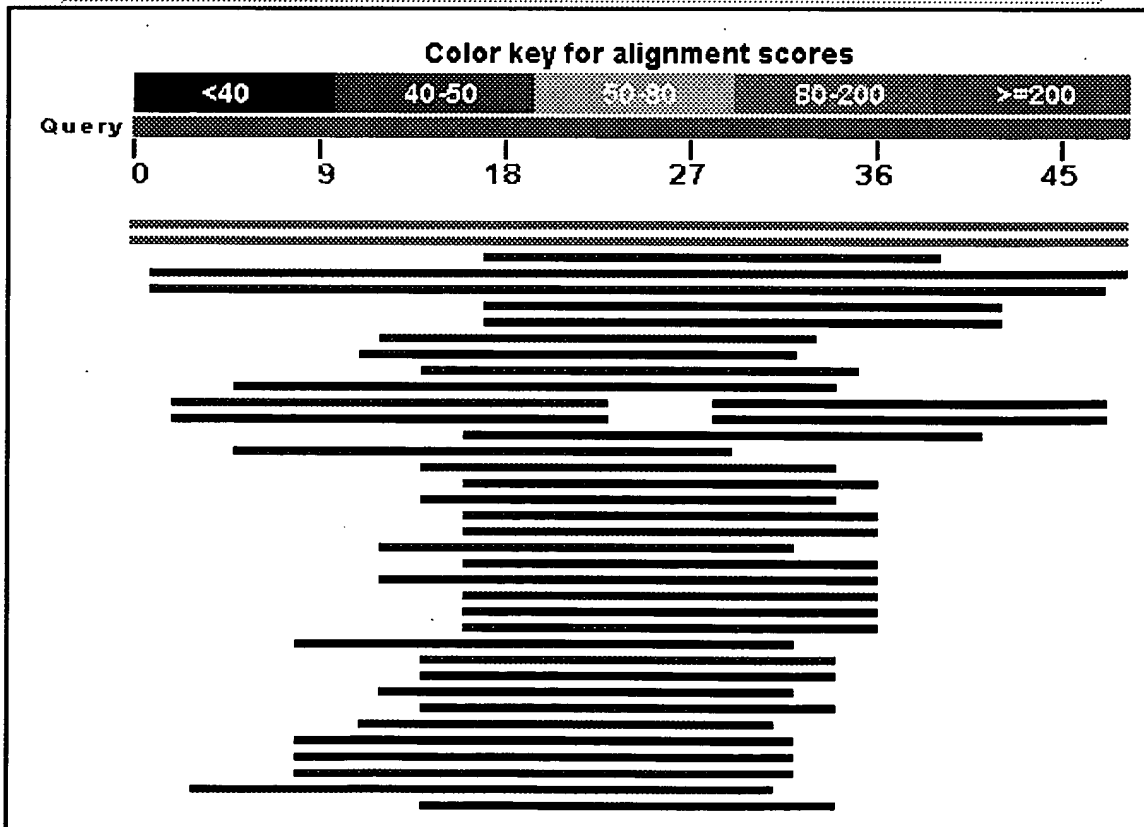
**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
3,413,089 sequences; 14,885,149,293 total letters

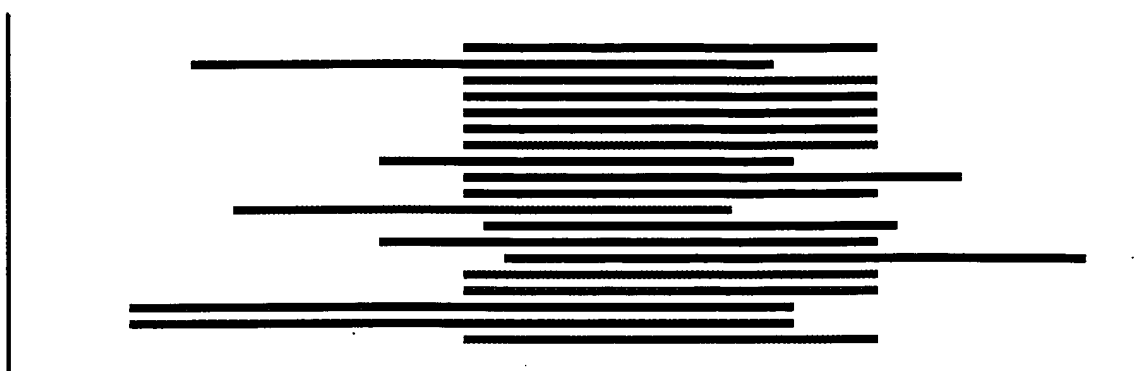
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

### Taxonomy reports

## Distribution of 102 Blast Hits on the Query Sequence


Mouse-over to show defline and scores, click to show alignments





Sequences producing significant alignments:			Score (Bits)	E Value
<a href="#">gi 4103165 gb AF021919.1 AF021919</a>	Actinobacillus pleuropneumo...		95.6	7e-18
<a href="#">gi 4103979 gb AF030511.1 AF030511</a>	Actinobacillus pleuropneumo...		87.7	2e-15
<a href="#">gi 18098529 gb AC093716.3 </a>	Homo sapiens BAC clone RP11-702L4 fro		44.1	0.022
<a href="#">gi 14550318 gb AC015933.9 </a>	Homo sapiens chromosome 18, clone CTD		44.1	0.022
<a href="#">gi 21281558 gb AC110015.5 </a>	Homo sapiens chromosome 18, clone ...		44.1	0.022
<a href="#">gi 37060013 gb AC123876.5 </a>	Mus musculus BAC clone RP23-270P19...		42.1	0.087
<a href="#">gi 34740427 gb AC125373.4 </a>	Mus musculus BAC clone RP23-379A13...		42.1	0.087
<a href="#">gi 37651868 gb AC125065.3 </a>	Mus musculus BAC clone RP23-430G6 ...		42.1	0.087
<a href="#">gi 25168704 emb AL845507.8 </a>	Zebrafish DNA sequence from clone...		42.1	0.087
<a href="#">gi 31581035 dbj AP006404.1 </a>	Lotus corniculatus var. japonicus...		42.1	0.087
<a href="#">gi 17149788 gb AC098861.2 </a>	Homo sapiens BAC clone RP11-297J2 fro		42.1	0.087
<a href="#">gi 25075790 gb AC007546.6 </a>	Homo sapiens 12 BAC RP11-946P6 (Ro...		42.1	0.087
<a href="#">gi 15808547 gb AC093214.2 </a>	Homo sapiens chromosome 5 clone CTD-2		42.1	0.087
<a href="#">gi 15451667 gb AC016594.7 </a>	Homo sapiens chromosome 5 clone CTD-2		42.1	0.087
<a href="#">gi 165657 gb J03744.1 RABPLP2</a>	Rabbit myelin P2 mRNA, complete cd		42.1	0.087
<a href="#">gi 28626888 gb AC129302.3 </a>	Mus musculus BAC clone RP24-441C24...		40.1	0.34
<a href="#">gi 38044253 gb AC102368.6 </a>	Mus musculus chromosome 14, clone RP2		40.1	0.34
<a href="#">gi 15012100 gb BC010956.1 </a>	Homo sapiens fibroblast growth fac...		40.1	0.34
<a href="#">gi 33235829 gb AC145772.1 </a>	Pan troglodytes BAC clone RP43-14J20		40.1	0.34
<a href="#">gi 46518131 emb BX248323.8 </a>	Zebrafish DNA sequence from clone...		40.1	0.34
<a href="#">gi 32402490 gb AY331807.1 </a>	Homo sapiens N-acetyltransferase 2...		40.1	0.34
<a href="#">gi 4557782 ref NM_000015.1 </a>	Homo sapiens N-acetyltransferase ...		40.1	0.34
<a href="#">gi 70921875 ref XM_729101.1 </a>	hypothetical protein (PC105701.00.0		40.1	0.34
<a href="#">gi 55630291 ref XM_519631.1 </a>	PREDICTED: Pan troglodytes simil...		40.1	0.34
<a href="#">gi 70887900 gb AC151286.3 </a>	Mus musculus BAC clone RP23-368B8 ...		40.1	0.34
<a href="#">gi 28227 emb X14672.1 HSAACT</a>	Human gene for arylamine N-acetyltr		40.1	0.34
<a href="#">gi 7630158 emb AL353012.1 SPBC1711</a>	S.pombe chromosome II cosmid		40.1	0.34
<a href="#">gi 24211331 gb AC120051.5 </a>	Homo sapiens chromosome 8, clone RP11		40.1	0.34
<a href="#">gi 41582918 gb AE017202.1 </a>	Lactobacillus johnsonii NCC 533, s...		40.1	0.34
<a href="#">gi 39752574 emb BX664601.6 </a>	Zebrafish DNA sequence from clone...		40.1	0.34
<a href="#">gi 38323074 emb BX465190.4 </a>	Zebrafish DNA sequence from clone...		40.1	0.34
<a href="#">gi 28829570 gb AC117176.2 </a>	Dictyostelium discoideum chromosom...		40.1	0.34
<a href="#">gi 58696608 emb CR356236.12 </a>	Zebrafish DNA sequence from clon...		40.1	0.34
<a href="#">gi 41352298 gb AY531391.1 </a>	Schizaphis graminum mitochondrion, co		40.1	0.34
<a href="#">gi 27923645 gb AC137810.3 </a>	Homo sapiens chromosome 5 clone XXfos		40.1	0.34
<a href="#">gi 20198523 gb AC116333.2 </a>	Homo sapiens chromosome 5 clone CTD-2		40.1	0.34
<a href="#">gi 20197301 gb AC005171.3 </a>	Arabidopsis thaliana chromosome 2 ...		40.1	0.34
<a href="#">gi 19747134 gb AC074132.5 </a>	Homo sapiens chromosome 5 clone CTD-2		40.1	0.34
<a href="#">gi 19071579 gb AC025919.8 </a>	Homo sapiens chromosome 15 clone R...		40.1	0.34
<a href="#">gi 15809172 gb AC093831.3 </a>	Homo sapiens BAC clone RP11-401I19 fr		40.1	0.34

<a href="#">gi 18921296 qb AC093281.2 </a>	Homo sapiens chromosome 5 clone RP11-	<a href="#">40.1</a>	0.34	
<a href="#">gi 18056697 qb AC025062.6 </a>	Homo sapiens chromosome 8, clone RP11	<a href="#">40.1</a>	0.34	
<a href="#">gi 45501306 qb BC067218.1 </a>	Homo sapiens N-acetyltransferase 2...	<a href="#">40.1</a>	0.34	
<a href="#">gi 6457296 qb AF179626.1 AF179626</a>	Expression vector pGP100, comp	<a href="#">40.1</a>	0.34	
<a href="#">gi 219415 dbj D90042.1 HUMAACTA3</a>	Homo sapiens mRNA for arylam...	<a href="#">40.1</a>	0.34	
<a href="#">gi 219411 dbj D90040.1 HUMAACTA1</a>	Homo sapiens mRNA for arylam...	<a href="#">40.1</a>	0.34	
<a href="#">gi 46879303 qb AC091332.8 </a>	Mus musculus chromosome 17, clone RP2	<a href="#">40.1</a>	0.34	
<a href="#">gi 46309633 qb AC123880.18 </a>	Mus musculus chromosome 3, clone RP2	<a href="#">40.1</a>	0.34	
<a href="#">gi 2731603 qb AC003960.1 AC003960</a>	Human Cosmid g5129g129 from 7q	<a href="#">40.1</a>	0.34	
<a href="#">gi 24430263 emb AL928739.5 </a>	Mouse DNA sequence from clone RP2...	<a href="#">40.1</a>	0.34	
<a href="#">gi 23304094 emb AL672031.9 </a>	Mouse DNA sequence from clone RP2...	<a href="#">40.1</a>	0.34	
<a href="#">gi 26092098 dbj AK047329.1 </a>	Mus musculus 10 days neonate cere...	<a href="#">40.1</a>	0.34	
<a href="#">gi 15431246 qb AC068042.5 </a>	Homo sapiens BAC clone RP11-535B12 fr	<a href="#">40.1</a>	0.34	
<a href="#">gi 62460846 qb AC154717.2 </a>	Mus musculus BAC clone RP24-369E16...	<a href="#">40.1</a>	0.34	
<a href="#">gi 62123187 qb AC154187.2 </a>	Mus musculus BAC clone RP24-444N2 ...	<a href="#">40.1</a>	0.34	
<a href="#">gi 5059233 qb AF147845.1 AF147845</a>	Parapsilocephala sp. 28S ribos	<a href="#">40.1</a>	0.34	
<a href="#">gi 5059231 qb AF147843.1 AF147843</a>	Bonjeania sp. 1 28S ribosomal	<a href="#">40.1</a>	0.34	
<a href="#">gi 219877 dbj D10872.1 HUMHNAT32</a>	Humam h NAT allele 3-2 gene for	<a href="#">40.1</a>	0.34	
<a href="#">gi 219874 dbj D10871.1 HUMHNAT22</a>	Human h NAT allele 2-2 gene for	<a href="#">40.1</a>	0.34	
<a href="#">gi 219871 dbj D10870.1 HUMHNAT12</a>	Human h NAT allele 1-2 gene for	<a href="#">40.1</a>	0.34	
<a href="#">gi 30522935 qb AC123841.4 </a>	Mus musculus BAC clone RP23-400M7 ...	<a href="#">38.2</a>	1.4	
<a href="#">gi 23499682 qb AC121568.3 </a>	Mus musculus BAC clone RP23-226F18 fr	<a href="#">38.2</a>	1.4	
<a href="#">gi 70935945 ref XM_733896.1 </a>	hypothetical protein (PC000461.04.0	<a href="#">38.2</a>	1.4	
<a href="#">gi 13443441 emb AL445584.16 </a>	Human DNA sequence from clone RP...	<a href="#">38.2</a>	1.4	
<a href="#">gi 56542279 emb AL162415.16 </a>	Human DNA sequence from clone RP...	<a href="#">38.2</a>	1.4	
<a href="#">gi 41392246 emb AL139141.23 </a>	Human DNA sequence from clone RP...	<a href="#">38.2</a>	1.4	
<a href="#">gi 15282137 emb AL157783.15 </a>	Human DNA sequence from clone RP...	<a href="#">38.2</a>	1.4	
<a href="#">gi 35209654 emb BX530036.7 </a>	Zebrafish DNA sequence from clone...	<a href="#">38.2</a>	1.4	
<a href="#">gi 21263329 qb AC099818.2 </a>	Homo sapiens chromosome 8, clone RP11	<a href="#">38.2</a>	1.4	
<a href="#">gi 14277165 qb AC073581.23 </a>	Homo sapiens 8 BAC RP11-42902 (Ro...	<a href="#">38.2</a>	1.4	
<a href="#">gi 56798018 emb CR925830.3 </a>	Human DNA sequence from clone RP1...	<a href="#">38.2</a>	1.4	
<a href="#">gi 38044013 emb BX664609.6 </a>	Human DNA sequence from clone RP1...	<a href="#">38.2</a>	1.4	
<a href="#">gi 51234144 qb AY714780.1 </a>	Homo sapiens carboxypeptidase B2 (...	<a href="#">38.2</a>	1.4	
<a href="#">gi 68467483 ref XM_717082.1 </a>	hypothetical protein (Ca019_4965) m	<a href="#">38.2</a>	1.4	
<a href="#">gi 68467250 ref XM_717194.1 </a>	hypothetical protein (Ca019_12430)	<a href="#">38.2</a>	1.4	
<a href="#">gi 56550491 emb CR339043.11 </a>	Zebrafish DNA sequence from clon...	<a href="#">38.2</a>	1.4	
<a href="#">gi 56541872 emb BX324201.7 </a>	Zebrafish DNA sequence from clone...	<a href="#">38.2</a>	1.4	
<a href="#">gi 38524391 emb BX649534.9 </a>	Zebrafish DNA sequence from clone...	<a href="#">38.2</a>	1.4	
<a href="#">gi 61740788 qb AC149601.3 </a>	Medicago truncatula chromosome 7 B...	<a href="#">38.2</a>	1.4	
<a href="#">gi 19698727 qb AC084740.5 </a>	Homo sapiens BAC clone RP11-423E20 fr	<a href="#">38.2</a>	1.4	
<a href="#">gi 19881533 qb AC012047.8 </a>	Homo sapiens chromosome 10 clone RP11	<a href="#">38.2</a>	1.4	
<a href="#">gi 19774485 qb AC116310.2 </a>	Homo sapiens chromosome 5 clone RP11-	<a href="#">38.2</a>	1.4	
<a href="#">gi 19774306 qb AC112918.3 </a>	Homo sapiens X BAC RP11-370L12 (Ro...	<a href="#">38.2</a>	1.4	
<a href="#">gi 18056717 qb AC104068.3 </a>	Homo sapiens BAC clone RP11-252F15 fr	<a href="#">38.2</a>	1.4	
<a href="#">gi 18482313 qb AC104791.3 </a>	Homo sapiens BAC clone RP11-181K12 fr	<a href="#">38.2</a>	1.4	
<a href="#">gi 48926772 qb AC133092.4 </a>	Mus musculus BAC clone RP23-404G6 ...	<a href="#">38.2</a>	1.4	
<a href="#">gi 68068246 ref XM_670941.1 </a>	Plasmodium berghei conserved hyp...	<a href="#">38.2</a>	1.4	
<a href="#">gi 68064473 ref XM_669129.1 </a>	Plasmodium berghei hypothetical ...	<a href="#">38.2</a>	1.4	
<a href="#">gi 18151020 qb AC092054.2 </a>	Homo sapiens chromosome 3 clone RP11-	<a href="#">38.2</a>	1.4	
<a href="#">gi 18042465 qb AC080082.4 </a>	Homo sapiens BAC clone RP11-531D14 fr	<a href="#">38.2</a>	1.4	
<a href="#">gi 67010238 qb AC154596.2 </a>	Mus musculus BAC clone RP23-354C17...	<a href="#">38.2</a>	1.4	
<a href="#">gi 62988592 qb AC154586.2 </a>	Mus musculus BAC clone RP23-362L12...	<a href="#">38.2</a>	1.4	
<a href="#">gi 62868198 qb AC154363.2 </a>	Mus musculus BAC clone RP23-154K12...	<a href="#">38.2</a>	1.4	
<a href="#">gi 17223145 qb AC097263.6 </a>	Homo sapiens X BAC RP11-298C3 (Ros...	<a href="#">38.2</a>	1.4	
<a href="#">gi 16798968 qb AC099036.1 </a>	Drosophila melanogaster, chromosom...	<a href="#">38.2</a>	1.4	
<a href="#">gi 16648483 qb AY060468.1 </a>	Drosophila melanogaster SD05282 full	<a href="#">38.2</a>	1.4	
<a href="#">gi 53748780 emb CR376826.12 </a>	Zebrafish DNA sequence from clon...	<a href="#">38.2</a>	1.4	


<a href="#">gi 52839510 emb CR293511.11 </a>	Zebrafish DNA sequence from clon...	<a href="#">38.2</a>	<a href="#">1.4</a>	
<a href="#">gi 24762667 ref NM_138087.3 </a>	Drosophila melanogaster CG13586-PA	<a href="#">38.2</a>	<a href="#">1.4</a>	
<a href="#">gi 15808550 gb AC093289.2 </a>	Homo sapiens chromosome 5 clone RP11-	<a href="#">38.2</a>	<a href="#">1.4</a>	

## Alignments

Get selected sequences

Select all


Deselect all

>  [gi|4103165|gb|AF021919.1|AF021919](#) Actinobacillus pleuropneumoniae MRP ATPase hor  
 RTX protein (apxIVA) genes, complete cds; and beta-galactosidase  
 (lacZ) gene, partial cds  
 Length=6736

Score = 95.6 bits (48), Expect = 7e-18  
 Identities = 48/48 (100%), Gaps = 0/48 (0%)  
 Strand=Plus/Plus

```



Query 1      ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  48
            |||
Sbjct 594    ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  641
  
```

>  [gi|4103979|gb|AF030511.1|AF030511](#) Actinobacillus pleuropneumoniae MRP ATPase hor  
 partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and  
 beta-galactosidase (lacZ) gene, partial cds  
 Length=7004

Score = 87.7 bits (44), Expect = 2e-15  
 Identities = 47/48 (97%), Gaps = 0/48 (0%)  
 Strand=Plus/Plus

```



Query 1      ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  48
            |||
Sbjct 605    ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAGACAAAATG  652
  
```

>  [gi|18098529|gb|AC093716.3|](#)  Homo sapiens BAC clone RP11-702L4 from 7, complete  
 Length=77028

Score = 44.1 bits (22), Expect = 0.022  
 Identities = 22/22 (100%), Gaps = 0/22 (0%)  
 Strand=Plus/Minus

```

Query 18     TATTTTATTAAATTTGAAAGGA  39
            |||
Sbjct 40143  TATTTTATTAAATTTGAAAGGA  40122
  
```


>  [gi|14550318|gb|AC015933.9|](#)  Homo sapiens chromosome 18, clone CTD-2023G8, comp]
 Length=249021

Score = 44.1 bits (22), Expect = 0.022  
 Identities = 25/26 (96%), Gaps = 0/26 (0%)  
 Strand=Plus/Minus

```


Query 2      TGAAATGTTAGTGAATTATTTTATT  27
  
```

|||||  
 Sbjct 42541 TGAAATGTTAGTGAATTATTGTTATT 42516

> [gi|21281558|gb|AC110015.5|](#)  Homo sapiens chromosome 18, clone RP11-104H13, comp  
 Length=168389


Score = 44.1 bits (22), Expect = 0.022  
 Identities = 25/26 (96%), Gaps = 0/26 (0%)  
 Strand=Plus/Minus

Query 2 TGAAATGTTAGTGAATTATTTTATT 27  
 |||||  
 Sbjct 102095 TGAAATGTTAGTGAATTATTGTTATT 102070

> [gi|37060013|gb|AC123876.5|](#)  Mus musculus BAC clone RP23-270P19 from chromosome  
 sequence  
 Length=203639


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 24/25 (96%), Gaps = 0/25 (0%)  
 Strand=Plus/Plus

Query 18 TATTTTATTAAATTTGAAAGGAAAC 42  
 |||||  
 Sbjct 29103 TATTTTATTAAATTTGAAAGGAAAC 29127

> [gi|34740427|gb|AC125373.4|](#)  Mus musculus BAC clone RP23-379A13 from chromosome  
 sequence  
 Length=190760


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 24/25 (96%), Gaps = 0/25 (0%)  
 Strand=Plus/Minus

Query 18 TATTTTATTAAATTTGAAAGGAAAC 42  
 |||||  
 Sbjct 6744 TATTTTATTAAATTTGAAAGGAAAC 6720

> [gi|37651868|gb|AC125065.3|](#)  Mus musculus BAC clone RP23-430G6 from chromosome  
 sequence  
 Length=205734


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 21/21 (100%), Gaps = 0/21 (0%)  
 Strand=Plus/Plus

Query 13 TGAATTATTTTATTAAATTTG 33  
 |||||  
 Sbjct 69284 TGAATTATTTTATTAAATTTG 69304

> [gi|25168704|emb|AL845507.8|](#)  Zebrafish DNA sequence from clone CH211-196F15, cc  
 Length=166074


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 21/21 (100%), Gaps = 0/21 (0%)  
 Strand=Plus/Minus

Query 12 GTGAATTATTTTATTAATTT 32  
 |||||  
 Sbjct 95258 GTGAATTATTTTATTAATTT 95238

> [gi|31581035|dbj|AP006404.1](#)  Lotus corniculatus var. japonicus genomic DNA, chi  
 clone:LjT43G19, TM0290, complete sequence  
 Length=125592


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 21/21 (100%), Gaps = 0/21 (0%)  
 Strand=Plus/Plus

Query 15 AATTATTTTATTAATTTGAA 35  
 |||||  
 Sbjct 42526 AATTATTTTATTAATTTGAA 42546

> [gi|17149788|gb|AC098861.2](#)  Homo sapiens BAC clone RP11-297J2 from 4, complete  
 Length=185791


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 27/29 (93%), Gaps = 0/29 (0%)  
 Strand=Plus/Minus

Query 6 ATGTTAGTGAATTATTTTATTAATTTGA 34  
 ||||| |  
 Sbjct 27117 ATGTTATTAATTATTTTATTAATTTGA 27089

> [gi|25075790|gb|AC007546.6](#)  Homo sapiens 12 BAC RP11-946P6 (Roswell Park Canc  
 Human BAC Library) complete sequence  
 Length=168396


Score = 42.1 bits (21), Expect = 0.087  
 Identities = 21/21 (100%), Gaps = 0/21 (0%)  
 Strand=Plus/Minus

Query 28 AATTTGAAAGGAAACAAAATG 48  
 |||||  
 Sbjct 93168 AATTTGAAAGGAAACAAAATG 93148

> [gi|15808547|gb|AC093214.2](#)  Homo sapiens chromosome 5 clone CTD-2060C23, comple  
 Length=148327

Score = 42.1 bits (21), Expect = 0.087  
 Identities = 21/21 (100%), Gaps = 0/21 (0%)  
 Strand=Plus/Plus

Query 3 GAAATGTTAGTGAATTATTTT 23  
 |||||  
 Sbjct 141378 GAAATGTTAGTGAATTATTTT 141398

> [gi|15451667|gb|AC016594.7|](#)  Homo sapiens chromosome 5 clone CTD-201003, complete  
Length=146235


Score = 42.1 bits (21), Expect = 0.087  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 3 GAAATGTTAGTGAATTATTTT 23  
|||||  
Sbjct 109754 GAAATGTTAGTGAATTATTTT 109774

> [gi|165657|gb|J03744.1|RABPLP2](#) Rabbit myelin P2 mRNA, complete cds  
Length=1836


Score = 42.1 bits (21), Expect = 0.087  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAAGGAAA 41  
|||||  
Sbjct 1314 TTATTTTATTCATTTGAAAGGAAA 1290

> [gi|28626888|gb|AC129302.3|](#)  Mus musculus BAC clone RP24-441C24 from chromosome  
sequence  
Length=186647


Score = 40.1 bits (20), Expect = 0.34  
Identities = 23/24 (95%), Gaps = 0/24 (0%)  
Strand=Plus/Minus

Query 6 ATGTTAGTGAATTATTTTATTAA 29  
|||||  
Sbjct 159817 ATGTTAGTGGATTATTTTATTAA 159794

> [gi|38044253|gb|AC102368.6|](#)  Mus musculus chromosome 14, clone RP23-220D8, complete  
Length=208781


Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 28 AATTTGAAAGGAAACAAAAT 47  
|||||  
Sbjct 62496 AATTTGAAAGGAAACAAAAT 62515

> [gi|15012100|gb|BC010956.1|](#)  Homo sapiens fibroblast growth factor 7 (keratinocyte growth factor), mRNA (cDNA clone MGC:13629 IMAGE:4282925), complete  
cds  
Length=1713


Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 15 AATTATTTTTATTAATTTGA 34  
|||||||  
Sbjct 1157 AATTATTTTTATTAATTTGA 1176

> [gi|33235829|gb|AC145772.1|](#)  Pan troglodytes BAC clone RP43-14J20 from 7, complete  
Length=165087


Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Minus

Query 17 TTATTTTTATTAATTTGAAA 36  
|||||||  
Sbjct 51663 TTATTTTTATTAATTTGAAA 51644

> [gi|46518131|emb|BX248323.8|](#)  Zebrafish DNA sequence from clone CH211-199J6, complete  
Length=177714


Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 15 AATTATTTTTATTAATTTGA 34  
|||||||  
Sbjct 50137 AATTATTTTTATTAATTTGA 50156

> [gi|32402490|gb|AY331807.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2) gene, complete cds  
Length=13180


Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Minus

Query 17 TTATTTTTATTAATTTGAAA 36  
|||||||  
Sbjct 11152 TTATTTTTATTAATTTGAAA 11133

> [gi|4557782|ref|NM\\_000015.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA  
Length=1276

Score = 40.1 bits (20), Expect = 0.34  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Minus

Query 17 TTATTTTTATTAATTTGAAA 36  
|||||||  
Sbjct 1189 TTATTTTTATTAATTTGAAA 1170

> [gi|70921875|ref|XM\\_729101.1|](#)  hypothetical protein (PC105701.00.0) mRNA, partial  
Length=641



Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 13 TGAATTATTTTATTAATTT 32  
 |||||  
 Sbjct 444 TGAATTATTTTATTAATTT 425

> [gi|55630291|ref|XM\\_519631.1|](#) **G** PREDICTED: Pan troglodytes similar to Arylamine N-acetyltransferase 2 (Arylamide acetylase 2) (Arylamine N-acetyltransferase, polymorphic) (PNAT) (N-acetyltransferase type 2) (NAT-2) (LOC464024), mRNA  
 Length=1598

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 1466 TTATTTTATTAATTTGAAA 1447

> [gi|70887900|gb|AC151286.3|](#) **B** Mus musculus BAC clone RP23-368B8 from chromosome 1  
 sequence  
 Length=178835

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Plus

Query 13 TGAATTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 95904 TGAATTATTTTATTAATTTGAAA 95927

> [gi|28227|emb|X14672.1|HSAACT](#) **EG** Human gene for arylamine N-acetyltransferase (H  
 Length=1891

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 1803 TTATTTTATTAATTTGAAA 1784


> [gi|7630158|emb|AL353012.1|SPBC1711](#) **B** S.pombe chromosome II cosmid c1711  
 Length=38000

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 17 TTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 17007 TTATTTTATTAATTTGAAA 17026


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 17 TTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 17595 TTATTTTATTAATTTGAAA 17614

> [gi|24211331|gb|AC120051.5|](#)  Homo sapiens chromosome 8, clone RP11-809L8, complete  
 Length=200827

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus


Query 17 TTATTTTATTAATTTGAAA 36  
 |||||  
 Sbjct 147211 TTATTTTATTAATTTGAAA 147230

> [gi|41582918|gb|AE017202.1|](#)  Lactobacillus johnsonii NCC 533, section 3 of 7 of  
 genome  
 Length=305337

Features in this part of subject sequence:  
hypothetical protein


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Minus

Query 9 TTAGTGAATTATTTTATTAATTT 32  
 |||||  
 Sbjct 39867 TTAGAGAATTATTTTATTAATTT 39844

> [gi|39752574|emb|BX664601.6|](#)  Zebrafish DNA sequence from clone CH211-135J1 in J  
 22, complete sequence  
 Length=76145


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 15 AATTATTTTATTAATTTGA 34  
 |||||  
 Sbjct 14454 AATTATTTTATTAATTTGA 14473

> [gi|38323074|emb|BX465190.4|](#)  Zebrafish DNA sequence from clone DKEY-121A11 in J  
 22, complete sequence  
 Length=183103


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 15 AATTATTTTTATTAATTTGA 34  
 |||||  
 Sbjct 31944 AATTATTTTTATTAATTTGA 31925

> [gi|28829570|gb|AC117176.2|](#)  Dictyostelium discoideum chromosome 2 map 5018074-  
 AX4, complete sequence  
 Length=182871


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 13 TGAATTATTTTTATTAATTT 32  
 |||||  
 Sbjct 32116 TGAATTATTTTTATTAATTT 32097

> [gi|58696608|emb|CR356236.12|](#)  Zebrafish DNA sequence from clone CH211-251P4 in  
 13, complete sequence  
 Length=171465


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 15 AATTATTTTTATTAATTTGA 34  
 |||||  
 Sbjct 51826 AATTATTTTTATTAATTTGA 51807

> [gi|41352298|gb|AY531391.1|](#)  Schizaphis graminum mitochondrion, complete genome  
 Length=15721


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 12 GTGAATTATTTTTATTAATT 31  
 |||||  
 Sbjct 7453 GTGAATTATTTTTATTAATT 7434

> [gi|27923645|gb|AC137810.3|](#)  Homo sapiens chromosome 5 clone XXfos-102B1, complete  
 Length=43668


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Minus

Query 9 TTAGTGAATTATTTTTATTAATTT 32  
 |||||  
 Sbjct 12473 TTAGTGAATTATTTATTATTAATTT 12450

> [gi|20198523|gb|AC116333.2|](#)  Homo sapiens chromosome 5 clone CTD-2242E19, complete  
 Length=112119


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Plus

Query 9 TTAGTGAATTATTTTATTATAATTT 32  
 |||||  
 Sbjct 27260 TTAGTGAATTATTTTATTATAATTT 27283

> [gi|20197301|gb|AC005171.3|](#)  Arabidopsis thaliana chromosome 2 clone T4E14 map  
 sequence  
 Length=138181


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Plus

Query 9 TTAGTGAATTATTTTATTATAATTT 32  
 |||||  
 Sbjct 110773 TTAGTAAATTATTTTATTATAATTT 110796

> [gi|19747134|gb|AC074132.5|](#)  Homo sapiens chromosome 5 clone CTD-2266L18, complete  
 sequence  
 Length=118131


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 26/28 (92%), Gaps = 0/28 (0%)  
 Strand=Plus/Plus

Query 4 AAATGTTAGTGAATTATTTTATTATAATTT 31  
 |||||  
 Sbjct 109572 AAATATTAATGAATTATTTTATTATAATTT 109599

> [gi|19071579|gb|AC025919.8|](#)  Homo sapiens chromosome 15 clone RP11-947024 map 15  
 sequence  
 Length=188439

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 15 AATTATTTTATTATAATTTGA 34  
 |||||  
 Sbjct 3774 AATTATTTTATTATAATTTGA 3793


> [gi|15809172|gb|AC093831.3|](#)  Homo sapiens BAC clone RP11-401I19 from 4, complete  
 sequence  
 Length=182116

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTATAATTTGAAA 36  
 |||||  
 Sbjct 9233 TTATTTTATTATAATTTGAAA 9214


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 17 TTATTTTATTATTAATTTGAAA 36  
 |||||  
 Sbjct 10365 TTATTTTATTATTAATTTGAAA 10384

> [gi|18921296|gb|AC093281.2|](#)  Homo sapiens chromosome 5 clone RP11-414H23, complete  
 Length=167455


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 26/28 (92%), Gaps = 0/28 (0%)  
 Strand=Plus/Plus

Query 4 AAATGTTAGTGAATTATTTTATTAAATT 31  
 |||| ||| |||||  
 Sbjct 35938 AAATATTAATGAATTATTTTATTAAATT 35965

> [gi|18056697|gb|AC025062.6|](#)  Homo sapiens chromosome 8, clone RP11-685B14, complete  
 Length=190459


Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36  
 |||||  
 Sbjct 190372 TTATTTTATTATTAATTTGAAA 190353

> [gi|45501306|gb|BC067218.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase)  
 mRNA (cDNA clone MGC:71963 IMAGE:4722596), complete cds  
 Length=1344

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36  
 |||||  
 Sbjct 1186 TTATTTTATTATTAATTTGAAA 1167

> [gi|6457296|gb|AF179626.1|AF179626](#)  Expression vector pGP100, complete sequence  
 Length=19012



Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36  
 |||||  
 Sbjct 15283 TTATTTTATTATTAATTTGAAA 15264

>  gi|219415|dbj|D90042.1|HUMAACTA3  Homo sapiens mRNA for arylamine N-acetyltransferase  
 cds  
 Length=1276



Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36  
 |||||  
 Sbjct 1189 TTATTTTATTAAATTTGAAA 1170

>  gi|219411|dbj|D90040.1|HUMAACTA1  Homo sapiens mRNA for arylamine N-acetyltransferase  
 cds  
 Length=1210



Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36  
 |||||  
 Sbjct 1123 TTATTTTATTAAATTTGAAA 1104

>  gi|46879303|gb|AC091332.8|  Mus musculus chromosome 17, clone RP23-12K1, complete  
 Length=216370



Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Plus

Query 13 TGAATTATTTTATTAAATTT 32  
 |||||  
 Sbjct 63589 TGAATTATTTTATTAAATTT 63608

>  gi|46309633|gb|AC123880.18|  Mus musculus chromosome 3, clone RP23-225M12, complete  
 Length=224562

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Plus

Query 17 TTATTTTATTAAATTTGAAAGGAA 40  
 |||||  
 Sbjct 166635 TTATTTTATTAAATTTGAAAGGAA 166658

>  gi|2731603|gb|AC003960.1|AC003960  Human Cosmid g5129g129 from 7q31.3, complete  
 Length=43593

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 20/20 (100%), Gaps = 0/20 (0%)  
 Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36

|||||  
 Sbjct 28843 TTATTTTATTAATTTGAAA 28824

> ☐ [gi|24430263|emb|AL928739.5|](#) ☒ Mouse DNA sequence from clone RP23-409L24 on chr10  
 sequence  
 Length=153028

Score = 40.1 bits (20), Expect = 0.34  
 Identities = 23/24 (95%), Gaps = 0/24 (0%)  
 Strand=Plus/Plus

Query 6 ATGTTAGTGAATTATTTTATTAA 29  
 |||||  
 Sbjct 72495 ATGTTAGTGGATTATTTTATTAA 72518

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Aug 9, 2005 12:07 AM

Number of letters in database: 2,000,247,405

Number of sequences in database: 3,413,089

Lambda K H  
 1.37 0.711 1.31

Gapped  
 Lambda K H  
 1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 3413089

Number of Hits to DB: 3386291

Number of extensions: 280204

Number of successful extensions: 93444

Number of sequences better than 10: 123

Number of HSP's better than 10 without gapping: 123

Number of HSP's gapped: 93444

Number of HSP's successfully gapped: 124

Number of extra gapped extensions for HSPs above 10: 92053

Length of query: 48

Length of database: 14885149293

Length adjustment: 20

Effective length of query: 28

Effective length of database: 14816887513

Effective search space: 414872850364

Effective search space used: 414872850364

A: 0

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 12 (24.3 bits)

S2: 18 (36.2 bits)



# results of BLAST

# BLASTN 2.2.11 [Jun-05-2005]

# Query:

# Database: nr

# Fields: Query id, Subject id, % identity, alignment length, mismatches, gap openin

1_24169	gi 4103165 gb AF021919.1 AF021919	100.00	4004	0	0	2733
1_24169	gi 4103165 gb AF021919.1 AF021919	100.00	2677	0	0	1
1_24169	gi 4103979 gb AF030511.1 AF030511	97.94	2722	52	4	2733
1_24169	gi 4103979 gb AF030511.1 AF030511	97.09	1442	34	8	5299
1_24169	gi 4103979 gb AF030511.1 AF030511	99.14	1277	11	0	1401
1_24169	gi 4103979 gb AF030511.1 AF030511	87.57	1360	98	58	1
1_24169	gi 6671147 gb AF188867.1 AF188867	100.00	391	0	0	6044
1_24169	gi 6671147 gb AF188867.1 AF188867	98.72	234	3	0	5219
1_24169	gi 6671147 gb AF188867.1 AF188867	97.35	151	4	0	4864
1_24169	gi 6671147 gb AF188867.1 AF188867	96.69	151	5	0	5689
1_24169	gi 6671147 gb AF188867.1 AF188867	91.67	156	9	4	4474
1_24169	gi 6671145 gb AF188866.1 AF188866	100.00	391	0	0	6044
1_24169	gi 6671145 gb AF188866.1 AF188866	98.72	234	3	0	5219
1_24169	gi 6671145 gb AF188866.1 AF188866	97.35	151	4	0	4864
1_24169	gi 6671145 gb AF188866.1 AF188866	96.69	151	5	0	5689
1_24169	gi 6671145 gb AF188866.1 AF188866	91.67	156	9	4	4474
1_24169	gi 6671143 gb AF188865.1 AF188865	100.00	391	0	0	6044
1_24169	gi 6671143 gb AF188865.1 AF188865	98.72	234	3	0	5219
1_24169	gi 6671143 gb AF188865.1 AF188865	97.35	151	4	0	4864
1_24169	gi 6671143 gb AF188865.1 AF188865	96.69	151	5	0	5689
1_24169	gi 6671143 gb AF188865.1 AF188865	91.67	156	9	4	4474
1_24169	gi 6671141 gb AF188864.1 AF188864	100.00	391	0	0	6044
1_24169	gi 6671141 gb AF188864.1 AF188864	98.72	234	3	0	5219
1_24169	gi 6671141 gb AF188864.1 AF188864	97.35	151	4	0	4864
1_24169	gi 6671141 gb AF188864.1 AF188864	96.69	151	5	0	5689
1_24169	gi 6671141 gb AF188864.1 AF188864	91.67	156	9	4	4474
1_24169	gi 6671139 gb AF188863.1 AF188863	100.00	391	0	0	6044
1_24169	gi 6671139 gb AF188863.1 AF188863	98.72	234	3	0	5219
1_24169	gi 6671139 gb AF188863.1 AF188863	97.35	151	4	0	4864
1_24169	gi 6671139 gb AF188863.1 AF188863	96.69	151	5	0	5689
1_24169	gi 6671139 gb AF188863.1 AF188863	91.67	156	9	4	4474
1_24169	gi 6671137 gb AF188862.1 AF188862	100.00	391	0	0	6044
1_24169	gi 6671137 gb AF188862.1 AF188862	98.72	234	3	0	5219
1_24169	gi 6671137 gb AF188862.1 AF188862	97.35	151	4	0	4864
1_24169	gi 6671137 gb AF188862.1 AF188862	96.69	151	5	0	5689
1_24169	gi 6671137 gb AF188862.1 AF188862	91.67	156	9	4	4474
1_24169	gi 6671135 gb AF188861.1 AF188861	100.00	391	0	0	6044
1_24169	gi 6671135 gb AF188861.1 AF188861	98.72	234	3	0	5219
1_24169	gi 6671135 gb AF188861.1 AF188861	97.35	151	4	0	4864
1_24169	gi 6671135 gb AF188861.1 AF188861	96.69	151	5	0	5689
1_24169	gi 6671135 gb AF188861.1 AF188861	91.67	156	9	4	4474
1_24169	gi 6671133 gb AF188860.1 AF188860	100.00	391	0	0	6044
1_24169	gi 6671133 gb AF188860.1 AF188860	98.72	234	3	0	5219
1_24169	gi 6671133 gb AF188860.1 AF188860	97.35	151	4	0	4864
1_24169	gi 6671133 gb AF188860.1 AF188860	96.69	151	5	0	5689
1_24169	gi 6671133 gb AF188860.1 AF188860	91.67	156	9	4	4474
1_24169	gi 6671129 gb AF188858.1 AF188858	100.00	391	0	0	6044
1_24169	gi 6671129 gb AF188858.1 AF188858	98.72	234	3	0	5219
1_24169	gi 6671129 gb AF188858.1 AF188858	97.35	151	4	0	4864
1_24169	gi 6671129 gb AF188858.1 AF188858	96.69	151	5	0	5689
1_24169	gi 6671129 gb AF188858.1 AF188858	91.67	156	9	4	4474
1_24169	gi 6671127 gb AF188857.1 AF188857	100.00	391	0	0	6044



1_24169	gi 6671127 gb AF188857.1 AF188857	98.72	234	3	0	5219
1_24169	gi 6671127 gb AF188857.1 AF188857	97.35	151	4	0	4864
1_24169	gi 6671127 gb AF188857.1 AF188857	96.69	151	5	0	5689
1_24169	gi 6671127 gb AF188857.1 AF188857	91.67	156	9	4	4474
1_24169	gi 6671131 gb AF188859.1 AF188859	96.94	392	10	2	6044
1_24169	gi 6671131 gb AF188859.1 AF188859	93.62	235	13	2	5219
1_24169	gi 6671131 gb AF188859.1 AF188859	91.19	159	12	2	4470
1_24169	gi 6671131 gb AF188859.1 AF188859	93.57	140	7	2	4876
1_24169	gi 6671131 gb AF188859.1 AF188859	92.86	140	8	2	5701
1_24169	gi 6671151 gb AF188869.1 AF188869	92.60	392	27	2	6044
1_24169	gi 6671151 gb AF188869.1 AF188869	89.04	228	23	2	5219
1_24169	gi 6671149 gb AF188868.1 AF188868	92.35	392	28	2	6044
1_24169	gi 6671149 gb AF188868.1 AF188868	89.04	228	23	2	5219
1_24169	gi 1655856 gb U62625.1 APU62625 99.16	119	0	1	6619	6736